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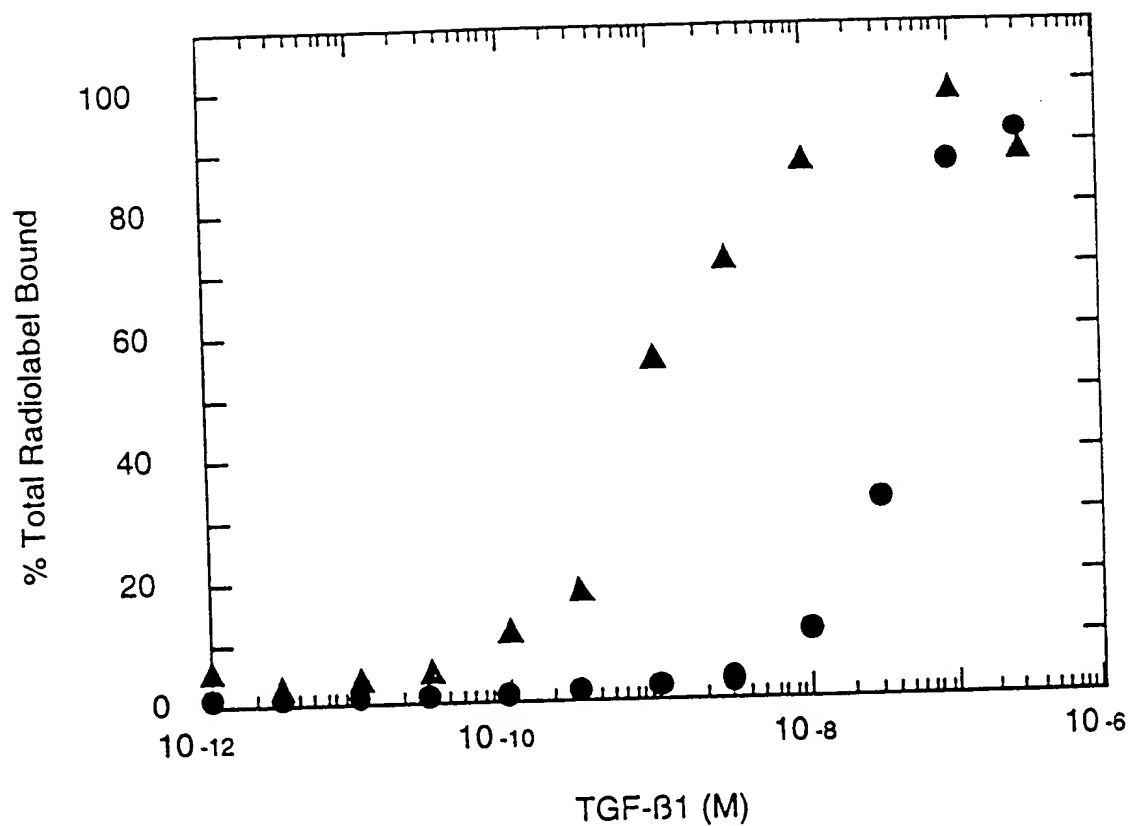


FIGURE 1

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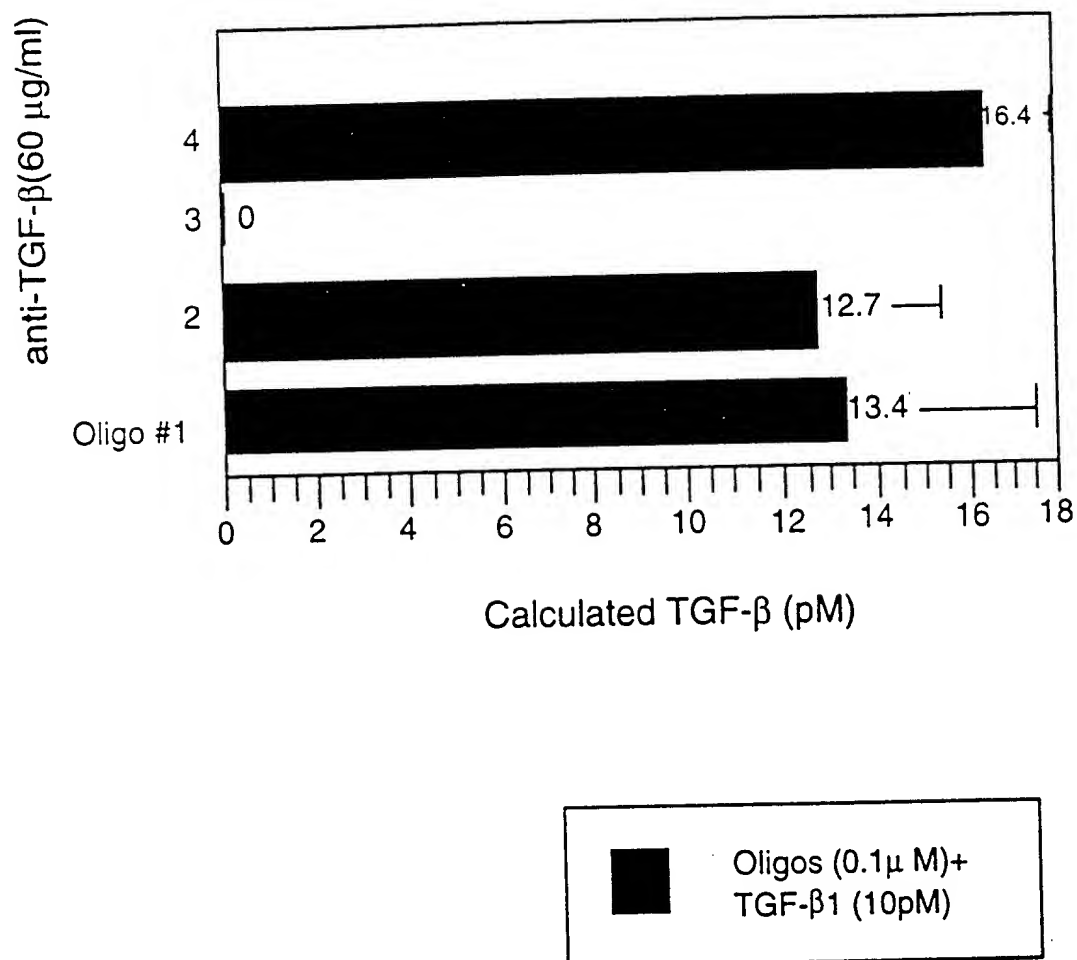
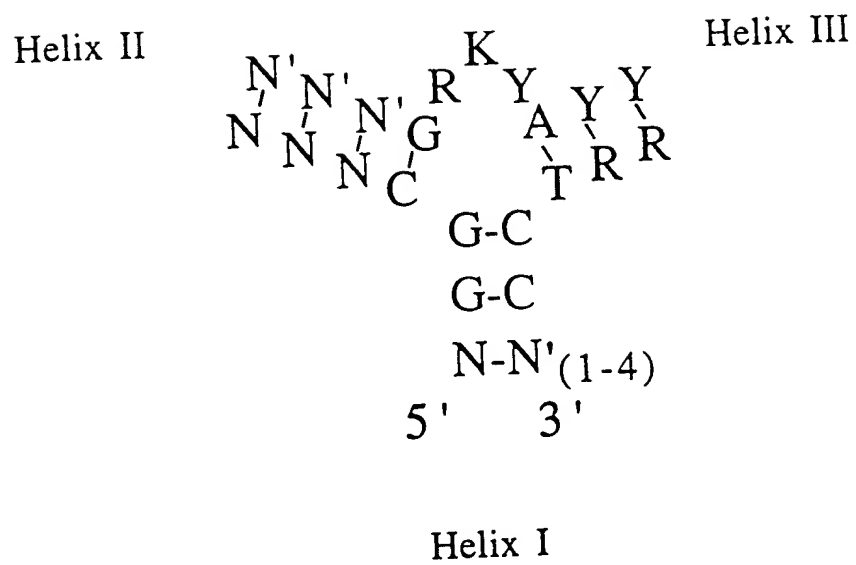


FIGURE 2

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SEQ ID NO: 171

FIGURE 3

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36t
 C C G T A G C T C A C
 G G C A T A G T A C
 G-C
 G-C
 A-T
 C-G
 A-T
 5'C-G[3'T]

SEQ ID NO: 173

20t
 C T T C G T G T C T T
 T T G C G T G A C T T
 G-C
 G-C
 5'TGGGA G-C G[3'T]

SEQ ID NO: 172

41t
 5' T A C T C A G C T G C A A G C
 [3'T] A T G A G T C G C A C T G T A
 G-C
 G-C
 G-C
 T A

SEQ ID NO: 174

FIGURE 4

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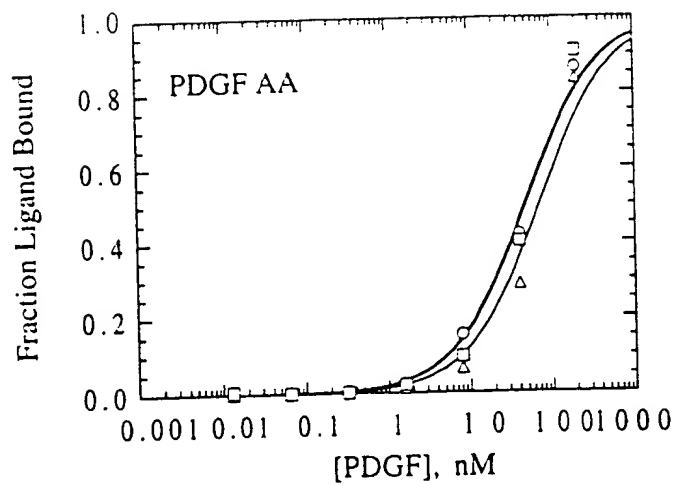


Figure 5A

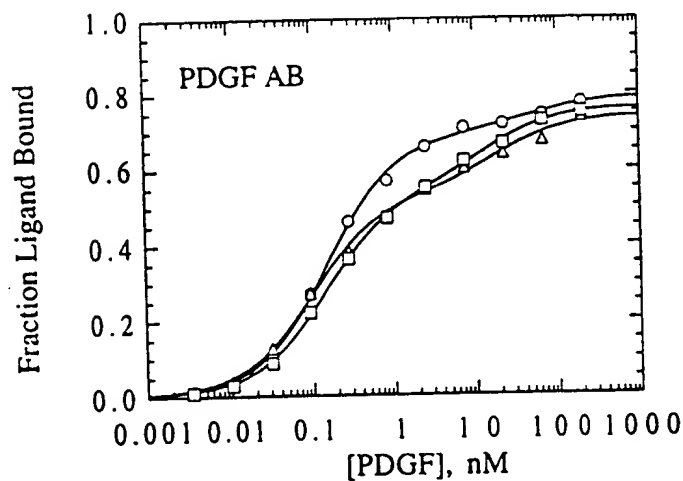


Figure 5B

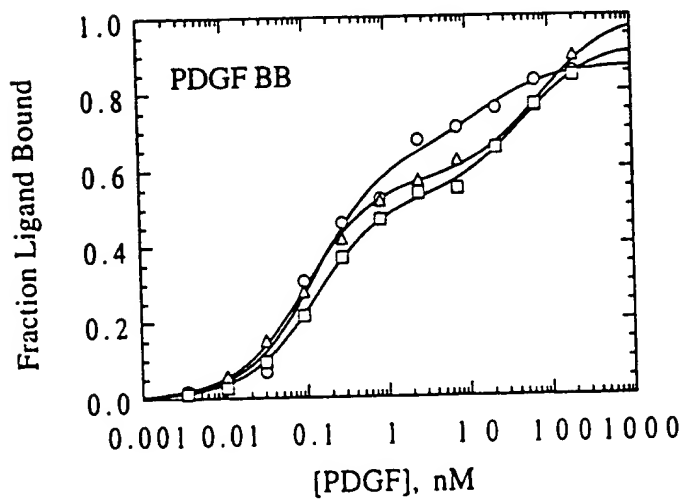


Figure 5C

SUBSTITUTE SHEET (RULE 26)

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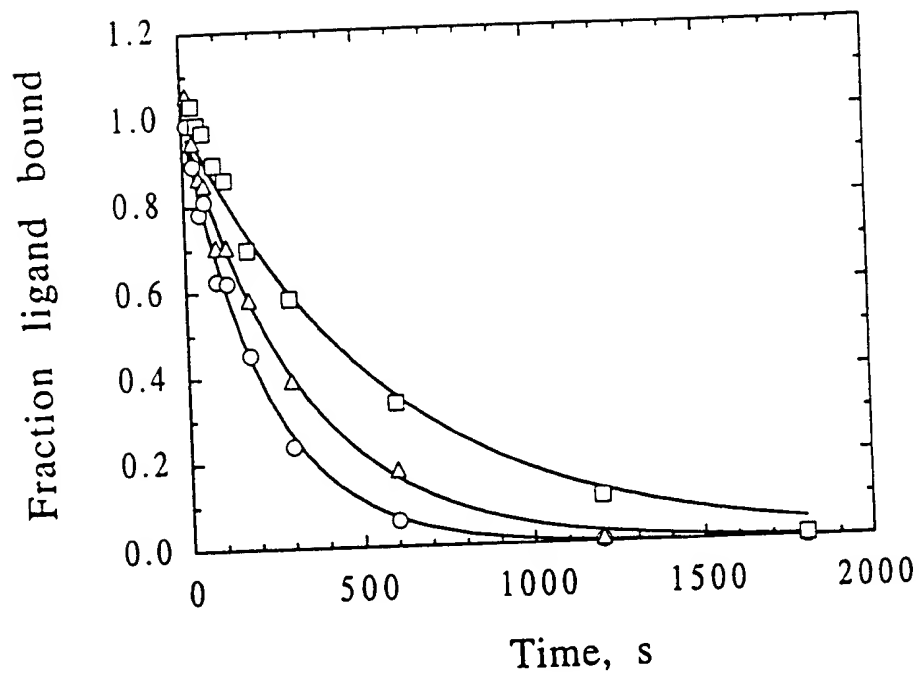


FIGURE 6

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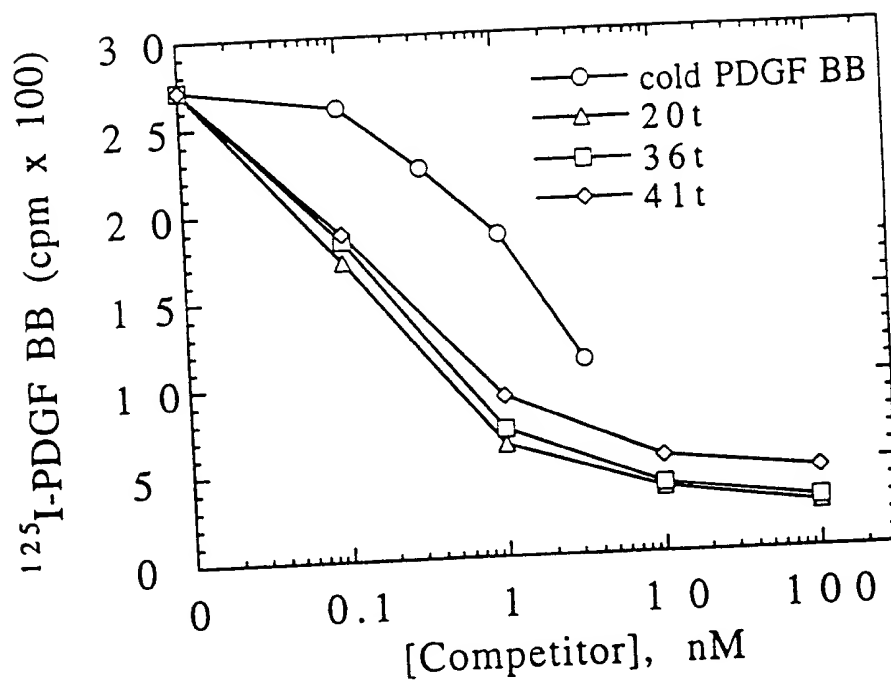


FIGURE 7

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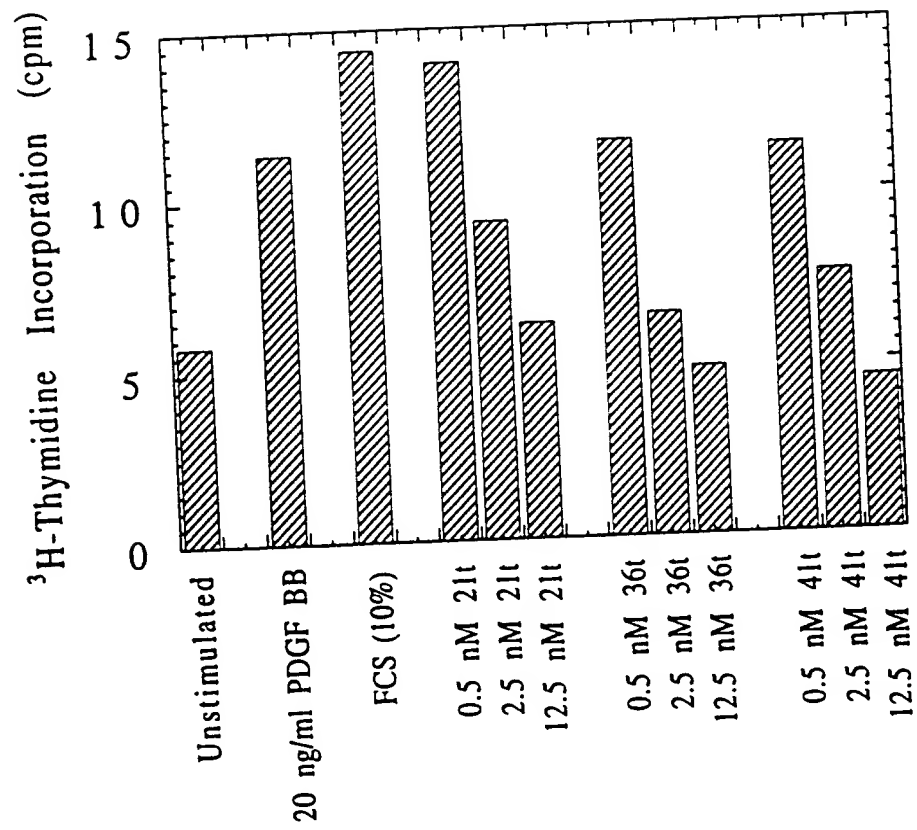
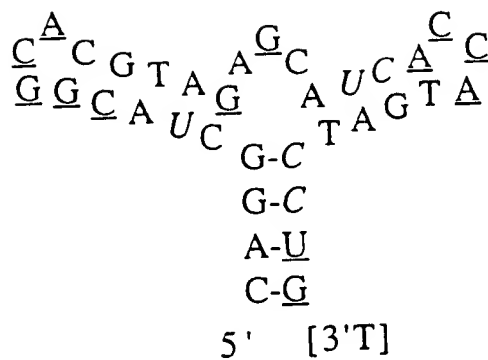
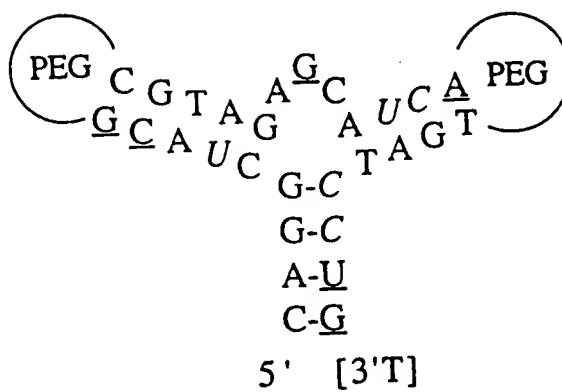


FIGURE 8

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 $K_d=0.065$ nM

SEQ ID NO: 175

 $K_d=0.097$ nM

SEQ ID NO: 176

FIGURE 9

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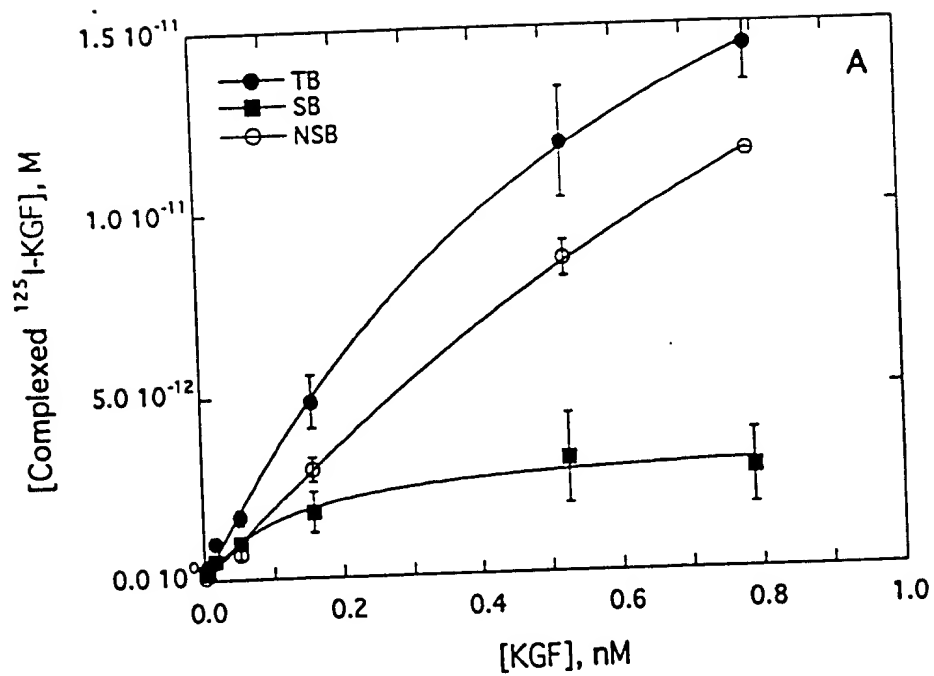


FIGURE 10A

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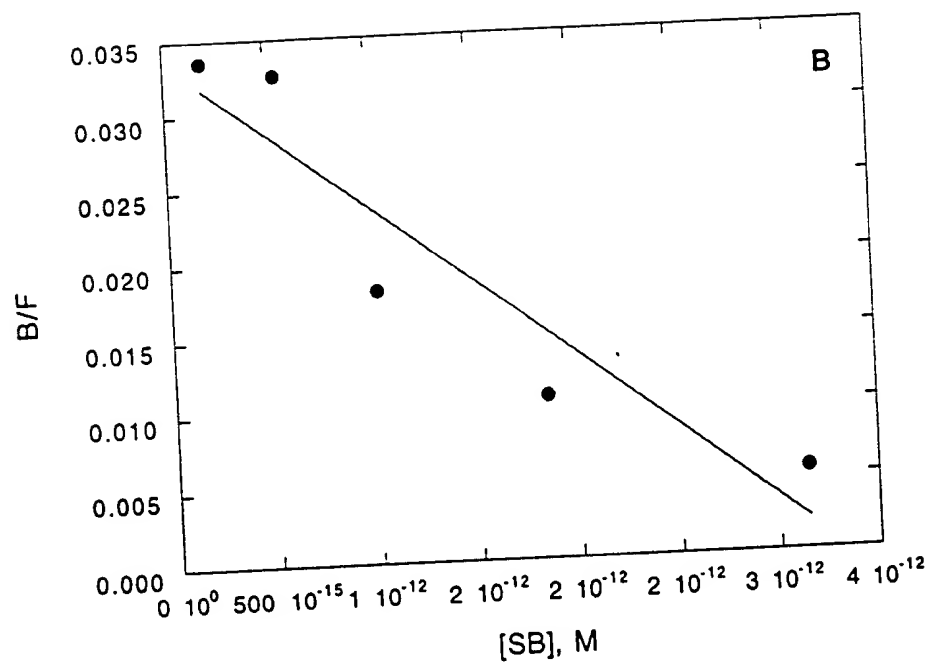


FIGURE 10B

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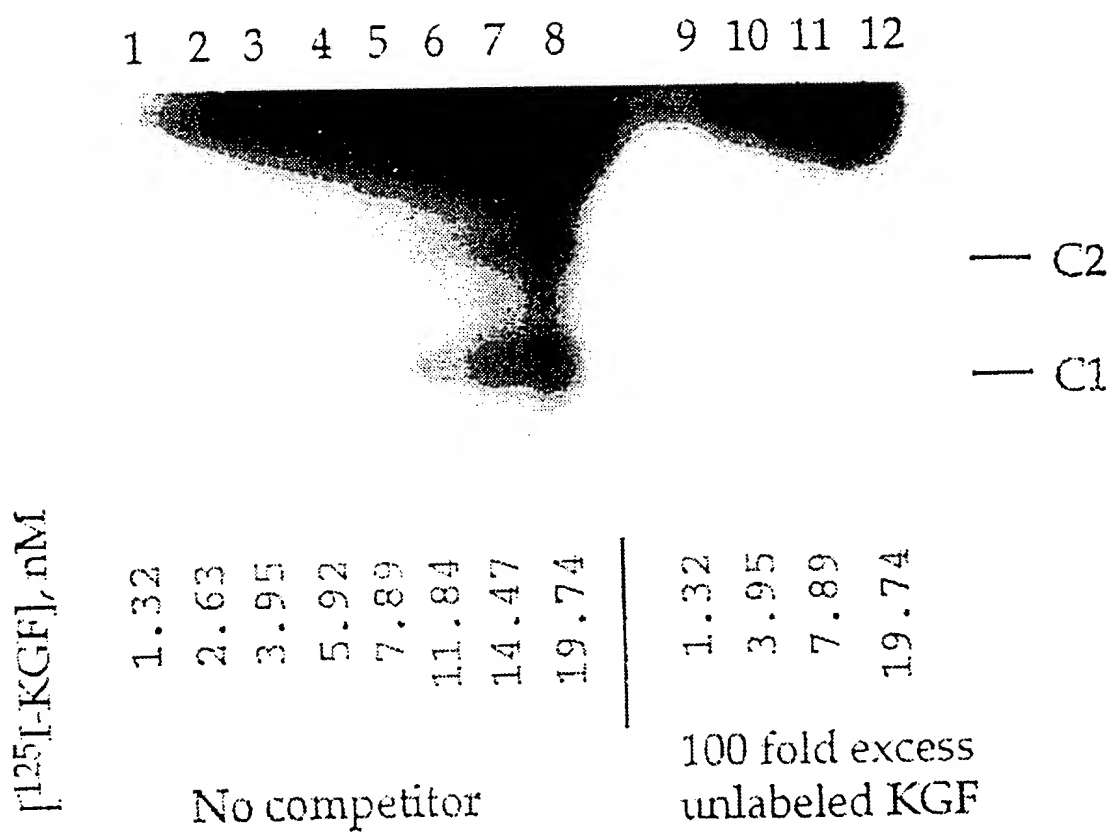


FIGURE 11

Class 1	SEQ ID NO:	Clone	Kd, nM	Ki, nM	5'-gGgagg	Summary Structure
231	*14F	gaaaga	0.001	3.3	acgaugcgagg	AAUUCUAAACUUUCU
223	*6F	gaaagaa	0.05	1.3	cgauugcg	GUGGCUUCUUGUAGACCC
232	*15F	gaaagagaa	0.07	6.7	augcggaug	ACAGUCUUC
259	*56F	gaaagagaa	0.07	0.3	augcggaug	AUUUKAUC
240	*26F	AACAGUCUG	0.23	0.3	GCAUUGGCCAUUAUGGCC	gacuc
246	37F	gaaagaa	0.46	6.7	GCCCGAUC	ACCGAATAC
233	*16F	gaaagaa	0.83		gacgaugcgga	AGCGCUUGACUAUACAAACN
249	42F	gaaagaa	0.9		acgaugcggaug	GAUUCUCCACACU
244	31F	gaaagaa	1.0		acgaugcggaug	UUCGCGUCCCGCag
245	35F	gaaagaa	1.1		acgaugcggaug	CCGUGCCcagacga
257	54F	gaaagaa	1.23		acgaugcggaug	GUUCCUUGCGCC
255	51F	gaaagaa	1.27		acgaugcggaug	CCGCGUCCCGcagac
220	2F	gaaagaa	1.77		acgaugcggaug	CUCUGCAGCAUUC
239	24F	gaaagaa	2.02		acgaugcggaug	gacgaucgacga
262	60F	gaaagaa	2.1		acgaugcggaug	CCGUGUGcagacga
238	23F	gaaagaa	2.52		acgaugcggaug	UCCUGC
222	5F	gaaagaa	2.53		acgaugcggaug	GAUAAACCUUCUGUGCCcagacga
225	8F	gaaagaa	2.63		acgaugcggaug	UCCUCCUGCCcaga
243	29F	gaaagaa	3.24		acgaugcggaug	CUCUGCCcagacga
224	7F	gaaagaa	3.69		acgaugcggaug	acgacucgcccga
252	45F	gaaagaa	4.7		acgaugcggaug	YYsYs
268						

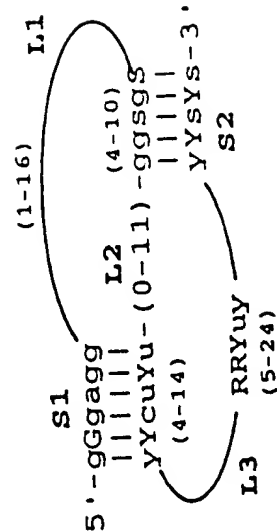


FIGURE 12A

Class 2

SEQ ID NO:	Clone	Kd, nM	Ki, nM	
230	*13P	0.03	10.0	<u>ggacga<u>uacaa</u></u>
254	*50P	0.12		<u>cga<u>uacaa</u>u<u>ga</u></u>
247	38P	0.33	0.2	<u>ggaa<u>aa</u>cga<u>u</u></u>
227	10F	0.47	10.0	<u>ga<u>aa</u>aa</u>
226	9F	0.83		<u>ggacga<u>uacaa</u></u>
256	53P	0.7		<u>aa<u>aa</u></u>
253	49F	1.0		<u>ga<u>aa</u>aa<u>ca</u>aa<u>uac</u></u>
250	43P	1.13	16.7	<u>aa<u>aa</u></u>
260	57P	1.2		<u>aaacga<u>u</u>ga</u>
248	41P	1.44		<u>ggagacga<u>u</u></u>
241	27P	1.52		<u>ggagga<u>ca</u>aa</u>
235	20P	2.05		<u>ua<u>aa</u>aa<u>g</u>ua</u>
258	55P	2.52		<u>aa<u>aa</u></u>
261	58P	2.52		<u>ga<u>aa</u>aa</u>
221	3P	4.47		<u>aa<u>aa</u>aaacga<u>u</u></u>
236	21P	ND		<u>aa<u>aa</u>aa<u>aa</u>ca</u>
242	28P	ND		<u>ggaa<u>aa</u></u>
269	Consensus			<u>tgGrrg</u>

Summary Structure

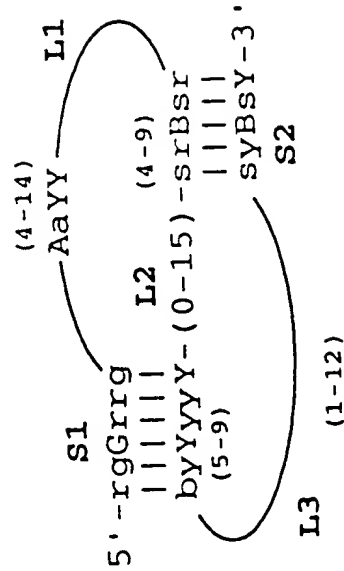


FIGURE 12B

Class 1							
SEQ ID NO:	Clone	Kd, nM	KI, nM				
195	14N	0.4	2.0	UCCAGGGAU	UGAAGUGUCGGGUAGGAACA	UAAAG	GCGGCca
199	25N	0.9		augcgga	GGGAUG	CAACUA	GCAGAUACCAGCUGGCCagacga
191	4N	0.7	23.3	augcgguugug	AAGAGG	UAAAGAUACCACGG	CCcagac
189	1N	0.5	16.7	gAAAGGG	ACCAUAAAG	CAACAA	GUGGUGGCCcaga
205	36N	8.27		gga	ggaugcgga	UAAAG	ACAAGUCGAACAAAG
203	34N	0.8		augcgggcg	AAGAGCU	CAGUC	ACAGUC
207	42N	0.8	266.7	augcgggcg	ACCU	CA CU	GCGGCCag
196	16N	1.4		cgauugcgga	AGUUCUACAAAGUUGGAA	Yaa	UGUacaga
				GGG	aa	gA	CCC
				Consensus			

Summary Structure

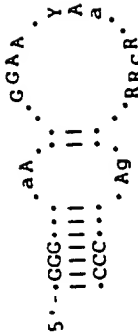


FIGURE 12C

Class 2	SEQ ID NO	Clone	K _d , nM	K _i , nM	AGGAAGGUCAGAGGAAA gacgaugcgg AGAAAGAUCCA ugcgggCUUAG acgaugcggc	CAGC GUGGAAGA GGAACAGCGAAA GGAAA AGGAGCAA	UGAG UGUU UGUU	CGUU CCGGUCG UGCGU CUGAG	CGGG IGCAGU CGGG GUGG GUGG CGGC	GUGcagacga AAUGUGAC ccagacgac Ucagacgac agacgacuc	cucgcccga ACUGGGGca ucgcccga ucgcccga gcccga	CGAA GACC	AGCCCCCUGGUGGU	ygay
209	47N		1.8											
198	24N		1.2											
202	29N		0.43	13.3										
204	35N		2.3											
192	6N		0.7	26.7										
190	2N		0.8	66.7										
211	54N		5.3											
271		Consensus												

Summary Structure

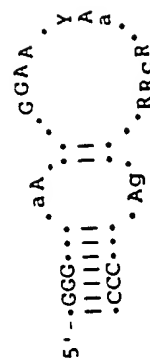


FIGURE 12D

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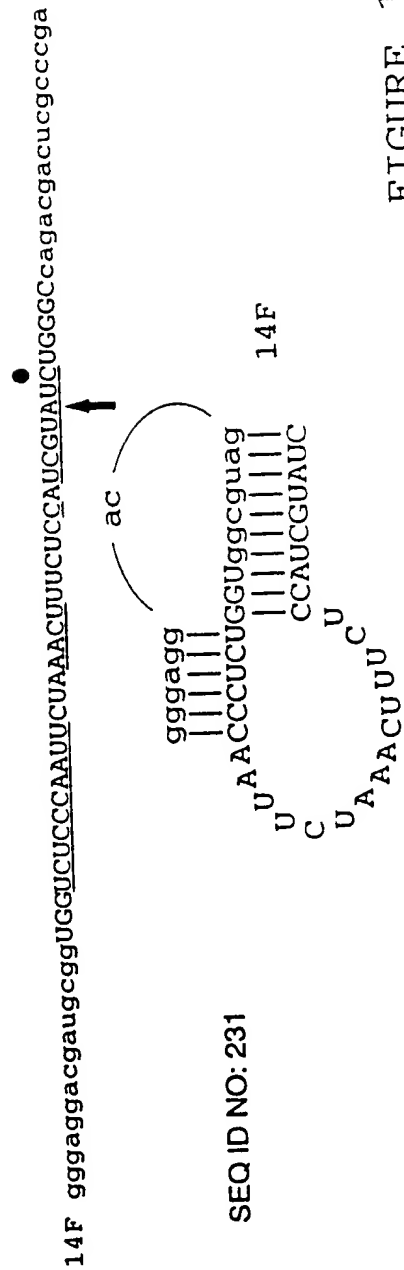
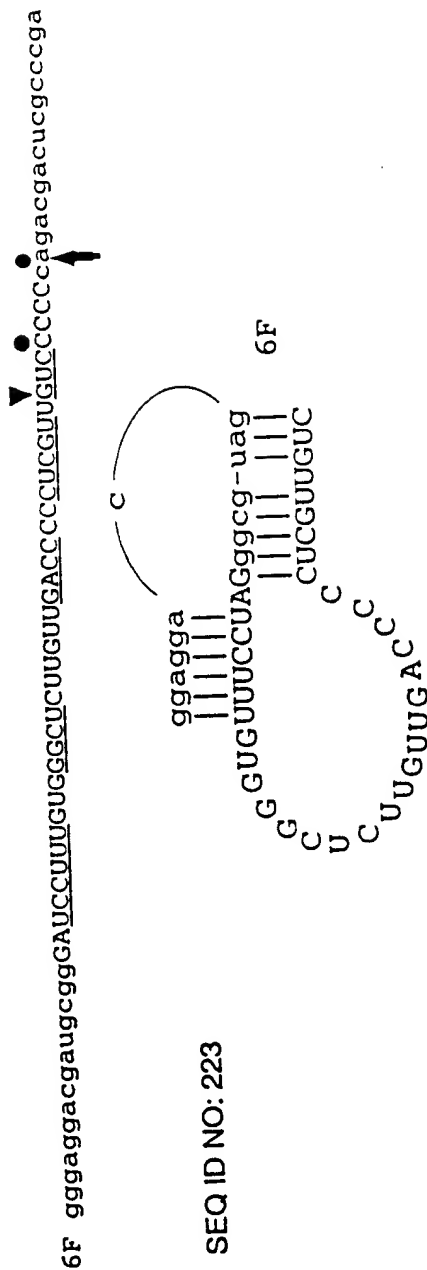


FIGURE 13